

Amendments to the Claims

Claim 1 (Original): An isolated polynucleotide encoding a protein having expansin activity wherein said polynucleotide hybridizes under high stringency conditions corresponding to 6X SSC, 50% formamide and 42° C, and washing at 0.2 X SSC at 65° C with the complement of the sequence set forth in SEQ ID NO:1.

Claim 2 (Original): The polynucleotide of claim 1, wherein said polynucleotide comprises at least 90% sequence identity to SEQ ID NO:1.

Claim 3 (Original): A polynucleotide comprising a DNA sequence that encodes a polypeptide having at least 90% sequence identity and that retains similar biological activity as the unmodified sequence of SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6 and SEQ ID NO:7.

Claim 4 (Original): A polynucleotide which encodes an expansin polypeptide, said polypeptide capable of restoring endogenous cell wall extension activity of heat inactivated cell walls and wherein said polynucleotide hybridizes under high stringency conditions corresponding to 6X SSC, 50% formamide and 42° C, and washing at 0.2 X SSC at 65° C with SEQ ID NO:1.

Claim 5 (Original): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:  
obtaining an oligonucleotide of about 4-30 contiguous bases derived from SEQ ID NO:1;

using said oligonucleotide to identify target nucleotide sequences through a hybridization, or PCR based assay, wherein said sequences are suspected to encode a protein with expansin activity; and thereafter assaying the protein encoded by said target nucleotide sequence for expansin activity.

**Claim 6 (Original):** The method of claim 5 wherein said oligonucleotide is a PCR primer.

**Claim 7 (Original):** The method of claim 5 wherein said oligonucleotide is a hybridization probe.

**Claim 8 (Original):** A nucleotide sequence which encodes upon expression a protein with expansin activity and wherein said sequence is identified by the method of claim 5.

**Claim 9 (Original):** A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:  
obtaining an oligonucleotide fragment of about 4-30 contiguous bases which encode contiguous amino acids from SEQ ID NOS:2-6;  
using said fragment to identify target polypeptide sequences through a hybridization or PCR based assay; and thereafter assaying a protein encoded by said polypeptide for expansin activity.

**Claim 10 (Original):** A polypeptide sequence identified by the method of claim 9.

Claim 11 (Original): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising:

designing a primer to amplify expansin encoding DNA based upon SEQ ID NO:7;

amplifying a cDNA fragment from said primer;

screening a cDNA library to identify a full length coding sequence of an expansin protein.

Claim 12 (Original): A nucleotide sequence which encodes upon expression a protein with expansin activity, said sequence identified by the method of claim 11.

Claim 13 (Currently amended): A method of identifying a nucleic acid which encodes upon expression an expansin protein comprising:

obtaining an oligonucleotide of about 4 to about 30 contiguous bases derived from SEQ ID NO:1;

using said oligonucleotide under high stringency conditions corresponding to 6X SSC, 50%

formamide and 42° C, and washing at 0.2 X SSC at 65° C to identity nucleic acids that

hybridizes under stringent conditions to SEQ ID NO:1 and wherein said polynucleotide encodes a protein suspected of having expansin activity; and thereafter,

assaying said polynucleotide-protein for expansin activity.

Claim 14 (Original): The method of claim 13, wherein said oligonucleotide is a PCR primer.

Claim 15 (Original): The method of claim 13, wherein said oligonucleotide is a hybridization probe.

Claim 16 (Currently amended): A method of identifying a nucleotide sequence which encodes upon expression an expansin protein comprising: obtaining an oligonucleotide fragment of about 4 to about 30 contiguous bases which encode contiguous amino acids from SEQ ID NOS:2-6; using said fragments under high stringency conditions corresponding to 6X SSC, 50% formamide and 42° C, and washing at 0.2 X SSC at 65° C to identify target polypeptide sequences; and thereafter, assaying said target polypeptide sequence for expansin activity.

Claim 17 (Original): A polypeptide sequence identified by the method of claim 16.